

FIGURE 1

TGMV Rep, amino acids 110-179:

TLVWGEFQVD GRSARGGCQT SNDAAAEALN ASSKEEALQI IREKIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:2)

Ala 1 mutant:

TLVWGEFQVD GAAAAGGCQT SNDAAAEALN ASSKEEALQI IREKIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:3)

Ala5 mutant:

TLVWGEFQVD GRSARGGCQT SNDAAAEALN ASSAAAAALQI IREKIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:15)

Ala4+5 mutant:

TLVWGEFQVD GRSARGGCQT SNDAAAAALA ASSAAAAALQI IREKIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:4)

Ala6 mutant:

TLVWGEFQVD GRSARGGCQT SNDAAAEALN ASSKEEALQI IAAAIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:5)

Ala7 mutant:

TLVWGEFQVD GRSARGGCQT SNDAAAEALN ASSKEEALQI IREKIPAAAL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:6)

Ala8 mutant:

TLVWGEFQVD GRSARGGCQT SNDAAAEALN ASSKEEALQI IREKIPEKYL FAFAALNSNL DRIFDKTPEP (SEQ ID NO:7)

Ala9 mutant:

TLVWGEFQVD GRSARGGCQT SNDAAAEALN ASSKEEALQI IREKIPEKYL FQFHNLSAL AAIFDKTPEP (SEQ ID NO:8)

Ala13 mutant:

TLVWGEAAVD GRSARGGCQT SNDAAAEALN ASSKEEALQI IREKIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:9)

Ala14 mutant:

TLVWGEFQVA GRSARGGCQT SNDAAAEALN ASSKEEALQI IREKIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:10)

Leu mutant:

TLVWGEFQVD GRSARGGCQT SNDLLLEALN ASSKEEALQI IREKIPEKYL FQFHNLSNL DRIFDKTPEP (SEQ ID NO:11)

Fig. 2A

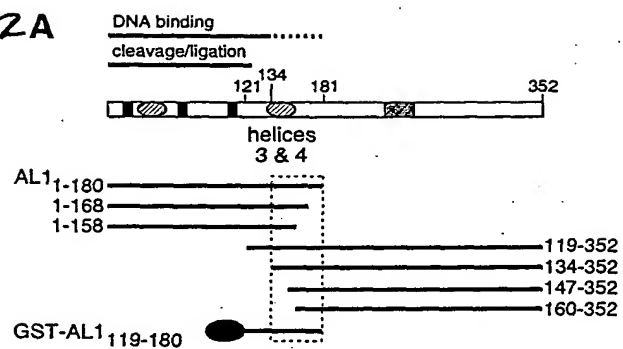


Fig. 2B

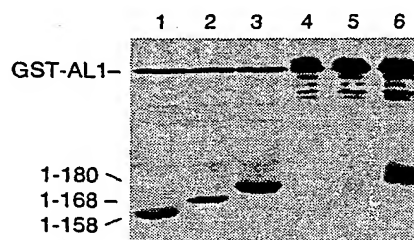


Fig. 2C

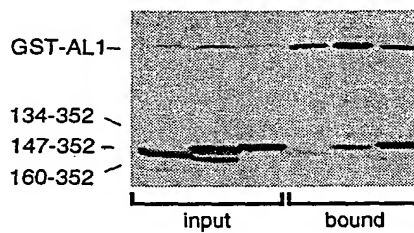
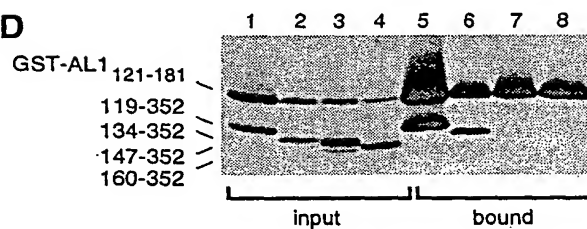


Fig. 2D



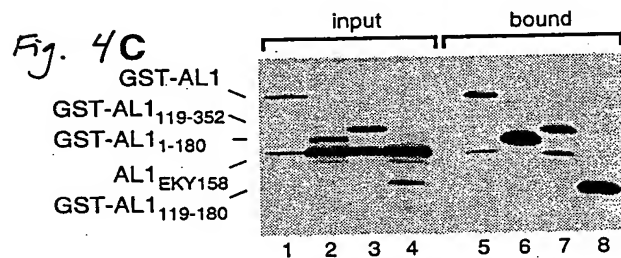
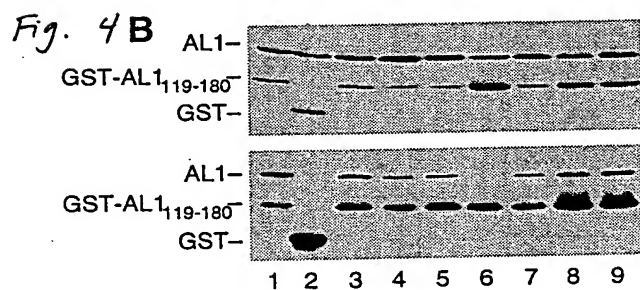


Fig. 5A

AL1/AL1

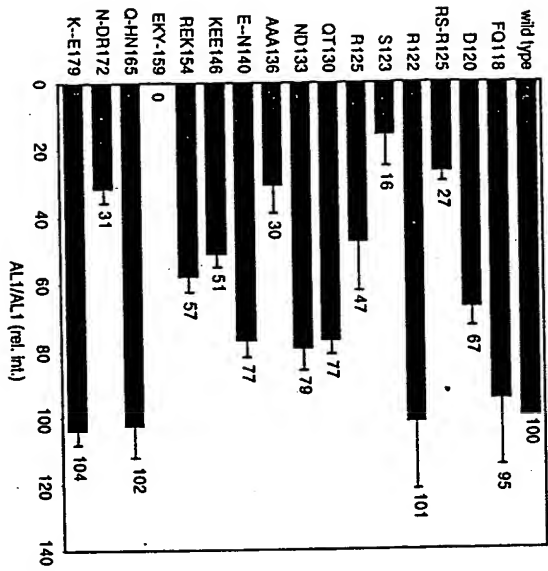


Fig. 5B

AL1/mRb

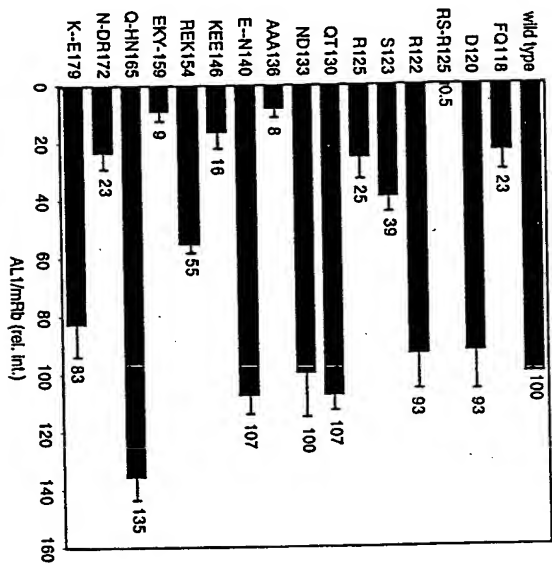


Fig. 6 A

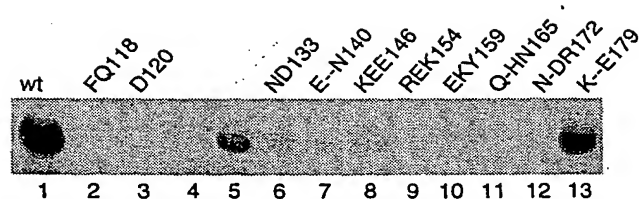


Fig. 6 B

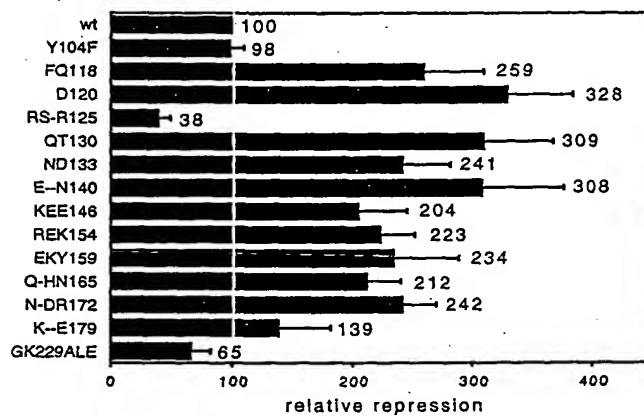


Fig. 7 A

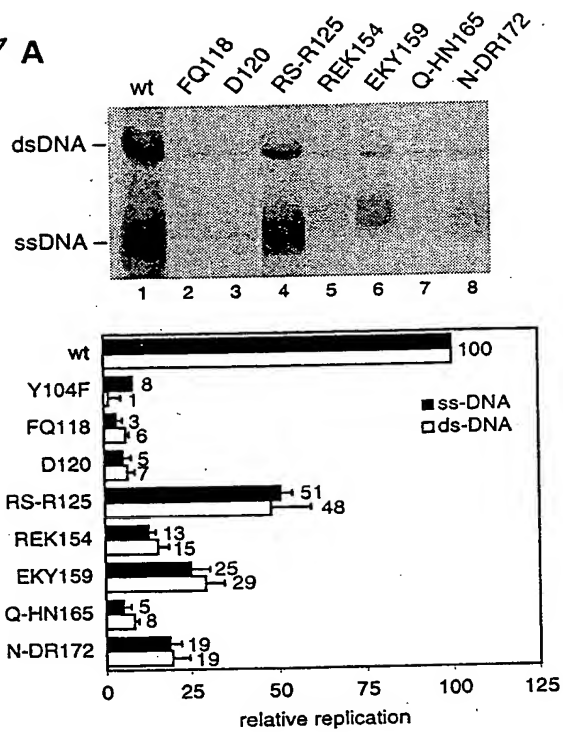


Fig. 7 B

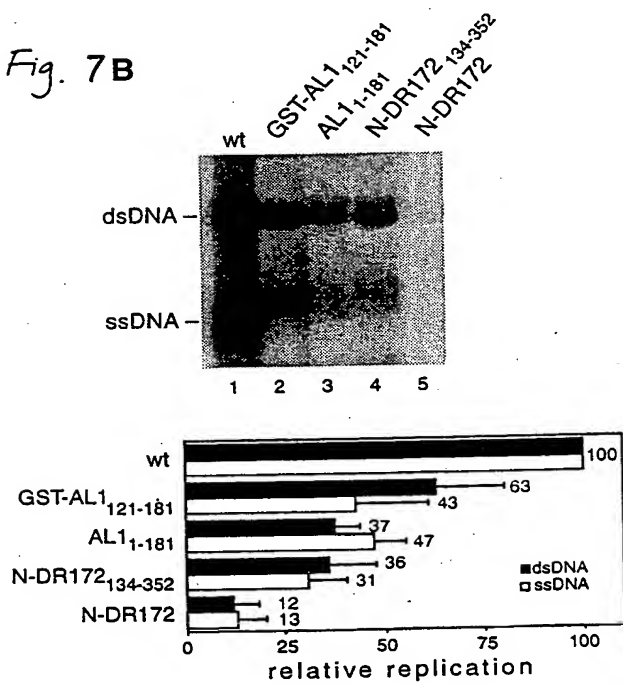


Fig. 8

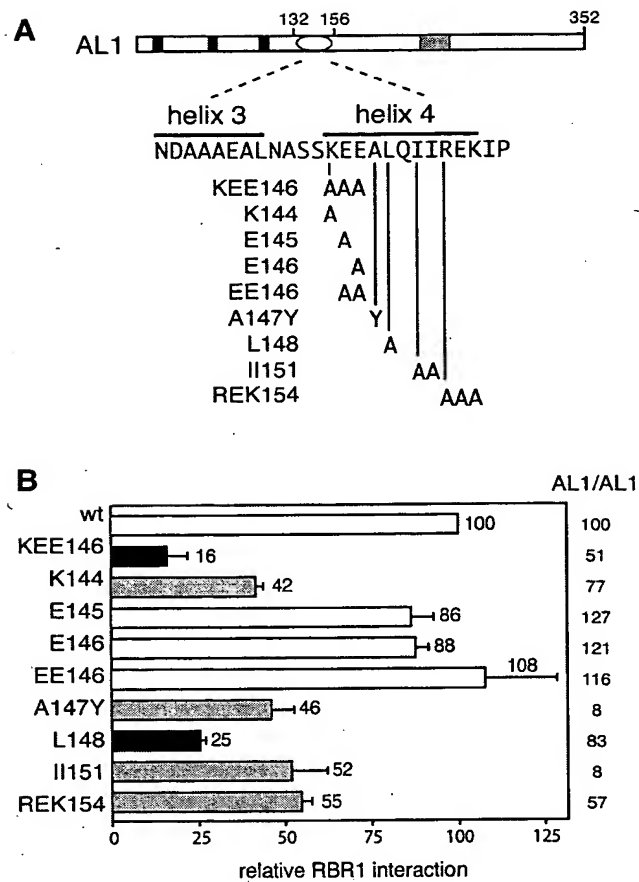


Fig. 9

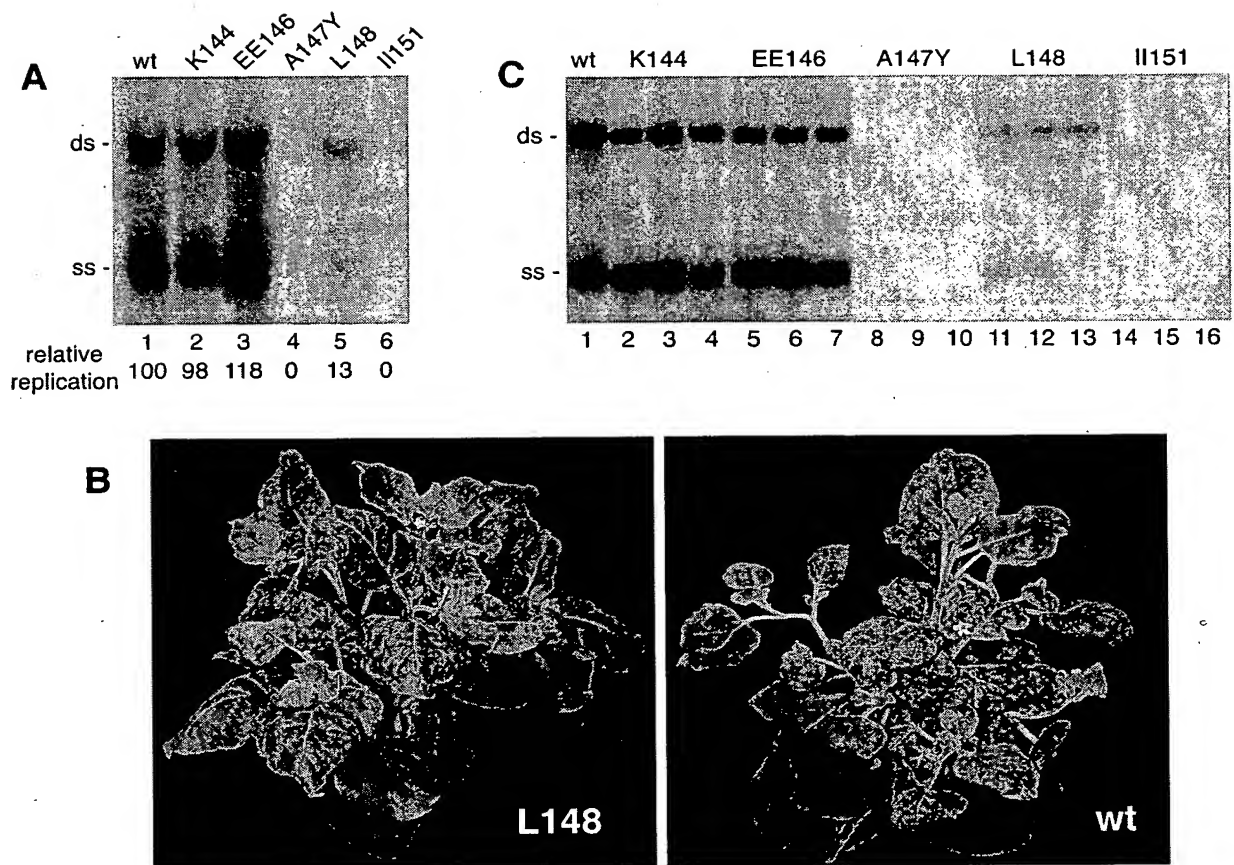


Fig.10

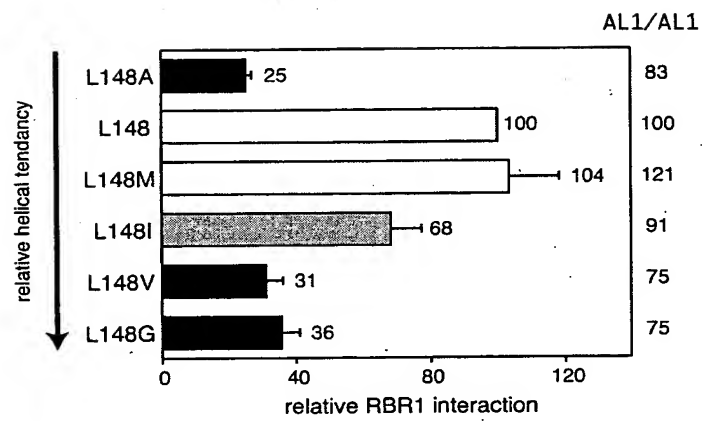
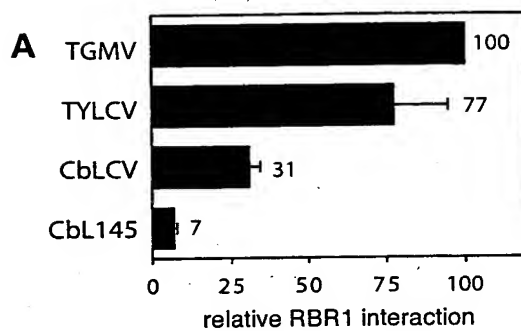


Fig. 11



B

helix 4

TGMV	KEEALQIIREKIP
TYLCV-DR	KSEALKILRELAP
CbLCV	VEEALAIIRAGDP
consensus	(±) ₁₋₃ $\overline{\text{AL}} \times \overline{\text{IIRE}} \times \times \text{P}$ $\text{M} \quad \text{VLK} \quad \text{D}$